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	Filing Date		2002-01-10	
	First Named Inventor	MARANAS, COSTAS D.		
	Art Unit	1631		
	Examiner Name	CLOW, LORI A.		
	Attorney Docket Number	P05468US01 - (2 OF 3)		

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1	Karp et al., "Ecocyc: Encyclopedia of Escherichia coli genes and metabolism," Nuc. Acids Res. 27:(1)55-58 (1999).	<input type="checkbox"/>
2	Kataoka et al., "Studies of hydrogen production by continuous culture system of hydrogen-producing anaerobic bacteria," Wat. Sci. Tech. 36:41-47 (1997).	<input type="checkbox"/>
3	Kauffman et al., "Advances in flux balance analysis," Curr. Opin. Biology. London, GB, 14(5):491-496 (2003).	<input type="checkbox"/>
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5	Kompala et al., GT, "Cybernetic Modeling of Microbial Growth on Multiple Substrates," Biotechnol. Bioeng. 26 (11):1272-1281 (1984).	<input type="checkbox"/>
6	Korotkova et al., "Poly-beta-hydroxybutyrate biosynthesis in the facultative methylotroph methylobacterium extorquens AM1: identification and mutation of gap11, gap20, and phaR," J. Bacteriol. 184(22):6174-6181 (2002).	<input type="checkbox"/>
7	Krieger et al., "MetaCyc: a multiorganism database of metabolic pathways and enzymes," Nucl. Acids Res. 32 (Database issue), D438-D4342 (2004).	<input type="checkbox"/>
8	Lutz et al., "Creating multiple-crossover DNA libraries independent of sequence identity," Proc. Natl. Acad. Sci. USA 98 (20):11248-11253 (2001).	<input type="checkbox"/>
9	Majewski and Domach, "Simple constrained-optimization view of acetate overflow in Escherichia coli," Biotechnol. Bioeng. 35(7):732-738 (1990).	<input type="checkbox"/>
10	McShan et al., "PathMiner: predicting metabolic pathways by heuristic search," Bioinformatics, 19(13):1692-1698 (2003).	<input type="checkbox"/>
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12	Methe et al., "Genome of Geobacter sulfurreducens: metal reduction in subsurface environments," Science 302 (5652):1967-9 (2003).	<input type="checkbox"/>
13	Misawa et al., "Production of beta-carotene in Zymomonas mobilis and Agrobacterium tumefaciens by introduction of the biosynthesis genes from Erwinia uredovora," Appl. Environ. Microbiol. 57(6):1847-1849 (1991).	<input type="checkbox"/>
14	Moore et al., "Predicting crossover generation in DNA shuffling," Proc. Natl. Acad. Sci. USA 98(6):3226-3231 (2001).	<input type="checkbox"/>
15	Moore and Maranas, "Modeling DNA Mutation and Recombination for Directed Evolution Experiments" J. Theor. Biol. 205(3):483-503 (2000).	<input type="checkbox"/>
16	Mushegian and Koonin, "A minimal gene set for cellular life derived by comparison of complete bacterial genomes," Proc. Natl. Acad. Sci. USA 93(19):10268-10273 (1996).	<input type="checkbox"/>
17	Nakamura and Whited, "Metabolic engineering for the microbial production of 1,3-propanediol," Curr. Opin. Biotechnol. 14(5):454-459 (2003).	<input type="checkbox"/>
18	Oh and Liao, "Gene expression profiling by DNA microarrays and metabolic fluxes in Escherichia coli," Biotechnol. Prog. 16(2):278-286 (2000).	<input type="checkbox"/>
19	Overbeek et al., "WIT: integrated system for high-throughput genome sequence analysis and metabolic reconstruction," Nucl. Acids. Res. 28(1):123-125 (2000).	<input type="checkbox"/>
20	Palsson, "The Challenges of in Silico Biology," Nat. Biotechnol. 18(11):1147-1150 (2000).	<input type="checkbox"/>
21	Papin et al., "Metabolic pathways in the post-genome era," Trends Biochem. Sci. 28(5):250-258 (2003).	<input type="checkbox"/>
22	Papoutsakis, "Equations and calculations for fermentations of butyric acid bacteria," Biotechnol. Bioeng. 26(2):174-187 (1984).	<input type="checkbox"/>

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23	Pennisi, "Laboratory Workhorse Decoded," Science 277:1432-1434 (1997).	<input type="checkbox"/>
24	Pharkya et al., "Exploring the overproduction of amino acids using the bilevel optimization framework OptKnock," Biotechnol. Bioeng. 84(7):887-899 (2003).	<input type="checkbox"/>
25	Price et al, "Genome-scale Microbial In Silico Models: The Constraints-Based Approach," Trends Biotechnol. 21 (4):162-169 (2003).	<input type="checkbox"/>
26	Quackenbush et al., "The TIGR Gene Indices: analysis of gene transcript sequences in highly sampled eukaryotic species," Nucleic Acids Res. 29:159-165 (2001).	<input type="checkbox"/>
27	Ramakrishna et al., "Cybernetic Modeling of Growth in Mixed, Substitutable Substrate Environments: Preferential and Simultaneous Utilization," Biotechnol. Bioeng. 52(1):141-151 (1996).	<input type="checkbox"/>
28	Ramakrishna et al., "Flux-balance analysis of mitochondrial energy metabolism: consequences of systemic stoichiometric constraints," Am. J. Physiol. Reg. Integr. Comp. Physiol. 280(3):R695-704 (2001).	<input type="checkbox"/>
29	Reed et al., "An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR)," Genome Biol. 4(9):R54 (2003).	<input type="checkbox"/>
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31	SantaLucia Jr., "A unified view of polymer, dumbbell, and oligonucleotide DNA nearest-neighbor thermodynamics," Proc. Natl. Acad. Sci. USA, 95(4):1460-1465 (1998).	<input type="checkbox"/>
32	Savageau, "Biochemical Systems Analysis," J. Theor. Biol. 25:365-369 (1969).	<input type="checkbox"/>
33	Schilling and Palsson, "Assessment of the metabolic capabilities of Haemophilus influenzae Rd through a genome-scale pathway analysis," J. Theor. Biol. 203(3):249-83 (2000).	<input type="checkbox"/>

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34	Schilling, et al, "Combining pathway analysis with flux balance analysis for the comprehensive study of metabolic systems," Biotechnol. Bioeng. 71(4):286-306 (2000).	<input type="checkbox"/>
35	Schilling, et al., "Genome-scale metabolic model of Helicobacter pylori 26695," J. Bacteriol. 184(16):4582-4593 (2002).	<input type="checkbox"/>
36	Schilling et al., "Toward metabolic phenomics: analysis of genomic data using flux balances," Biotechnol Prog, 15:288-295 (1999).	<input type="checkbox"/>
37	Segre et al., "Analysis of optimality in natural and perturbed metabolic networks," Proc Natl. Acad. Sci. USA 99 (23):15112-15117 (2002).	<input type="checkbox"/>
38	Segre et al., "From annotated genomes to metabolic flux models and kinetic parameter fitting," Omics, 7(3):301-316 (2003).	<input type="checkbox"/>
39	Selkov, et al., "MPW: the Metabolic Pathways Database," Nucl Acids Res, 26(1):43-45 (1998).	<input type="checkbox"/>
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45	Tomita, et al., "E-CELL: software environment for whole-cell simulation," Bioinformatics 15(1):72-84 (1999).	<input type="checkbox"/>
46	Tomita, "The E-Cell Project: Towards Integrative Simulation of cellular Processes," New Gen. Comput. 18:1-12 (2000).	<input type="checkbox"/>
47	Torres et al., "An Indirect Optimization Method for Biochemical Systems: Description of Method and Application to the Maximization of the Rate of Ethanol, Glycerol, and Carbohydrate Production in Saccharomyces cerevisiae," Biotechnol. Bioeng. 55(5):758-772 (1997).	<input type="checkbox"/>
48	Valdes et al., "Metabolic reconstruction of sulfur assimilation in the extremophile Acidithiobacillus ferrooxidans based on genome analysis," BMC Genomics 4:51 (2003).	<input type="checkbox"/>
49	Varma and Palsson, "Metabolic Capabilities of Escherichia coli: II. Optimal Growth Patterns," J. Theor. Biol. 165:503-522 (1993).	<input type="checkbox"/>
50	Varma and Palsson, "Metabolic Flux Balancing: Basic Concepts, Scientific and Practical Use," Biotechnol. 12:994-998 (1993).	<input type="checkbox"/>

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